

Rec'd PCT/PTO 13 SEP 2001

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In the Application of:

O. FAMODU ET AL.

CASE NO.: BB1270

APPLICATION NO.: 09/831,683

GROUP ART UNIT: UNKNOWN

INTERNATIONAL FILING DATE: 09 NOV 99 EXAMINER: UNKNOWN

FOR: PLANT AMINOACYL-tRNA SYNTHETASES

STATEMENT UNDER 37 CFR 1.821(g) and 1.825(b)

Assistant Commissioner for Patents
Washington, DC 20231

Sir:

The submission of the substitute Sequence Listing filed concurrently herewith does not include new matter.

The copy of the substitute Sequence Listing in computer readable form filed concurrently herewith is the same as the paper copy of the substitute Sequence Listing filed concurrently herewith.

Respectfully submitted,



Thomas M. Rizzo, Ph.D.
Attorney For Applicants
Registration No. 41,272
Telephone: 302-892-7760
Facsimile: 302-892-1026

Dated: August 8, 2001

SEQUENCE LISTING

<110> E. I. du Pont de Nemours and Company

<120> Plant Aminoacyl-tRNA Synthetases

<130> BB1270

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<150> 60/107,789

<151> 1998-November-10

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<212> DNA

<213> Zea mays

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Ala Cys Thr Asn Leu Leu Pro Asn Val Val Cys Glu Tyr Leu Tyr Asn
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<213> Oryza sativa

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<213> Oryza sativa

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Ser Val Phe Ser Arg Ile Arg Gly Ser Ala Thr Asn Phe Arg Asn Pro
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Met Ala Val Gly Gln Ala Ile Ala Asn Asn Leu Pro Gln Ser Asn Ile
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Ile Glu Ser Ile Ser Val Ala Gly Pro Gly Tyr Ile Asn Ile Thr Leu
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Ser Ser Asn Trp Ile Ala Gln Arg Ile Gln Asp Met Leu Val Cys Gly
100 105 110

Ile Lys Thr Trp Ala Pro Ile Leu Pro Val Lys Arg Ala Val Leu Asp
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165 170 175

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Lys Lys Arg Phe Asp Asp Pro Asp Phe Lys Glu Arg Ala Arg Gln
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Arg Leu Asn Val Lys Leu Glu Glu Lys Gly Glu Ser Phe Tyr Asn Pro
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Tyr Ile Pro Pro Val Leu Glu Glu Leu Thr Asn Lys Gly Leu Ile Val
275 280 285

Glu Ser Lys Gly Ala Arg Val Ile Phe Val Glu Asp His Pro Leu Ile
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Ala Leu Trp Tyr Arg Leu Asn Val Glu Lys Ala Glu Trp Ile Ile Tyr
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Ser Glu Ala Ile Gly Tyr Gly Ala Val Lys Tyr Ser Asp Leu Lys Asn
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Gln His Phe Asp Met Leu Phe Lys Ala Tyr Arg Arg Ala Gly Trp Leu
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Pro Lys Asp Glu Asn Ala Tyr Pro Lys Cys Thr His Ile Gly Phe Gly
65 70 75 80
Leu Val Leu Gly Glu Asp Gly Lys Arg Phe Arg Thr Arg Ser Ser Glu
85 90 95
Val Val Arg Leu Val Asp Leu Leu Asp Glu Ala Lys Arg Arg Cys Lys
100 105 110
Ile Ala Ile Leu Glu Arg Asp Thr Thr Lys Asp Trp Ser Glu Glu Glu
115 120 125
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130 135 140
Asp Leu Lys Ile Asn Arg Leu Thr Asn Tyr Thr Phe Asn Phe Asp Gln
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165 170 175
Ala Arg Ile Cys Ser Ile Ile Arg Lys Ser Gly Lys Asp Ile Glu Glu
180 185 190
Val Lys Arg Asn Gly Lys Ile Val Leu Asp His Glu Asp Glu Arg Ala
195 200 205
Leu Gly Leu His Leu Leu Gln Phe Pro Glu Val Phe Glu Glu Ala Cys
210 215 220
Thr Asn Leu Leu Pro Asn Phe Leu Cys Glu Tyr Leu Tyr Asn Leu Ala
225 230 235 240
Glu Ile Phe Thr Lys Lys Phe Tyr Ala Asn Cys Gln Val Val Gly Ser
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Leu Gly Asp Leu Leu Asp Glu Ala Lys Ser Arg Ser Lys Ser Glu Leu
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Leu Gln Arg Leu Thr Glu Asn Gly Lys Ile Val Asp Trp Thr Asp Glu
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Glu Leu Glu Gln Thr Ser Lys Ala Val Gly Tyr Gly Ala Val Lys Tyr
85 90 95
Ala Asp Leu Lys Asn Asn Arg Leu Thr Asn Tyr Thr Phe Ser Phe Asp
100 105 110
Gln Met Leu Ser Asp Lys Gly Asn Thr Ala Val Tyr Leu Gln Tyr Ala
115 120 125
His Ala Arg Ile Cys Ser Ile Ile Arg Lys Ser Asn Met Asp Val Glu
130 135 140
Glu Leu Lys Val Ser Gly Asn Ile Ser Leu Ala His Pro Asp Glu Arg
145 150 155 160

Val Leu Gly Leu Tyr Leu Ile Arg Tyr Ala Glu Ile Val Glu Glu Ala
165 170 175

Cys Thr Asn Leu Leu Pro Ser Val Leu Cys Glu Tyr Leu Tyr Asn Leu
180 185 190

Ser Glu Met Phe Thr Arg Phe Tyr Thr Asn Cys Gln Val Val Gly Ser
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<212> DNA

<213> Zea mays

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35 40 45

Leu His Gly Val Asn Pro Ile Ile Leu Tyr Ile Ala Arg Gly Ala Ser
50 55 60

Ile Ala Ser Leu Ser Gly Lys Asn Asp Ile Glu Phe Gly His Val Val
65 70 75 80

Glu Trp Leu Glu Tyr Ala Pro Thr Phe Leu Ser Gly Ser Glu Phe Glu
85 90 95

Asn Ala Cys Leu Phe Val Asp Gly Phe Leu Ala Ser Arg Thr Phe Leu
100 105 110

Val Gly His Gly Leu Thr Ile Ala Asp Ile Ala Val Trp Ser Asn Leu
115 120 125

Ala Gly Ile Gly Gln Arg Trp Glu Ser Leu Arg Lys Ser Lys Lys Tyr
130 135 140

Gln Asn Leu Val Arg Trp Phe Asn Ser Ile Asp Ser Glu Tyr Lys Glu
145 150 155 160

Ala Leu Asn Glu Val Val Ala Ala Phe Val Gly Lys Arg Gly Ile Gly
165 170 175

Lys Ser Pro Ala Pro Ser Leu Lys Glu Lys Val His Asp Ser Lys Asp
180 185 190

Pro Ser Ala Pro Glu Val Asp Leu Pro Gly Ala Lys Val Gly Lys Val
195 200 205

Cys Val Arg Phe Ala Pro Glu Pro Ser Gly Tyr Leu His Ile Gly His
210 215 220

Ala Lys Ala Ala Leu Leu Asn Lys Tyr Phe Ala Glu Arg Tyr Gln Gly
225 230 235 240

Arg Leu Ile Val Arg Phe Asp Asp Thr Asn Pro Ser Lys Glu Ser Asn
245 250 255

Glu Phe Val Glu Asn Leu Leu Lys Asp Ile Glu Thr Leu Gly Ile Lys
260 265 270

Tyr Asp Ala Val Thr Tyr Thr Ser Asp Tyr Phe Pro Lys Leu Met Glu
275 280 285

Met Ala Glu Ser Leu Ile Lys Gln Gly Lys Ala Tyr Ile Asp Asp Thr
290 295 300

Pro Lys Glu Gln Met Arg Lys Glu Arg Met Asp Gly Ile Glu Ser Arg
305 310 315 320

Cys Arg Asn Asn Thr Val Glu Glu Asn Leu Ser Leu Trp Lys Glu Met
325 330 335

Val Asn Gly Thr Glu Arg Gly Met Gln Cys Cys Val Arg Gly Lys Leu
340 345 350

Asp Met Gln Asp Pro Asn Lys Ser Leu Arg Asp Pro Val Tyr Tyr Arg
355 360 365

Cys Asn Thr Asp Pro His His Arg Val Gly Ser Lys Tyr Lys Val Tyr
370 375 380

Pro Thr Tyr Asp Phe Ala Cys Pro Phe Val Asp Ala Leu Glu Gly Val
385 390 395 400

Thr His Ala Leu Arg Ser Ser Glu Tyr His Asp Arg Asn Ala Gln Tyr
405 410 415

Tyr Arg Ile Leu Gln Asp Met Gly Leu Arg Arg Val Glu Ile Tyr Glu
420 425 430

Phe Ser Arg Leu Asn Met Val Tyr Thr Leu Leu Ser Lys Arg Lys Leu
435 440 445

Leu Trp Phe Val Gln Asn Lys Lys Val Glu Asp Trp Thr Asp Pro Arg
450 455 460

Phe Pro Thr Val Gln Gly Ile Val Arg Arg Gly Leu Lys Val Glu Ala
465 470 475 480

Leu Ile Gln Phe Ile Leu Gln Gln Gly Ala Ser Lys Asn Leu Asn Leu
485 490 495

Met Glu Trp Asp Lys Leu Trp Thr Ile Asn Lys Lys Ile Ile Asp Pro
500 505 510

Val Cys Ala Arg His Thr Ala Val Leu Lys Asp Gln Arg Val Ile Phe
515 520 525

Thr Leu Thr Asn Gly Pro Glu Glu Pro Phe Val Arg Ile Leu Pro Arg
530 535 540

His Lys Lys Phe Glu Gly Ala Gly Lys Lys Ala Thr Thr Phe Ala Asn
545 550 555 560

Arg Ile Trp Leu Asp Tyr Ala Asp Ala Ala Ile Asn Lys Gly Glu
565 570 575

Glu Val Thr Leu Met Asp Trp Gly Asn Ala Ile Val Lys Glu Ile Lys
580 585 590

Val Glu Ser Gly Val Ile Thr Glu Leu Val Gly Glu Leu His Leu Glu
595 600 605

Gly Ser Val Lys Thr Thr Lys Leu Lys Ile Thr Trp Leu Ala Asp Ile
610 615 620

Glu Glu Leu Val Pro Leu Ser Leu Val Glu Phe Asp Tyr Leu Ile Ser
625 630 635 640

Lys Lys Lys Leu Glu Asp Glu Asp Phe Leu Asp Asn Leu Asn Pro
645 650 655

Cys Thr Arg Arg Glu Ile Pro Ala Leu Gly Asp Ala Asn Met Arg Asn
660 665 670

Ile Lys Arg Gly Glu Ile Ile Gln Leu Glu Arg Lys Gly Tyr Tyr Arg
675 680 685

Cys Asp Ala Pro Phe Ile Arg Ser Ser Lys Pro Val Val Leu Phe Ala
690 695 700

Ile Pro Asp Gly Arg Gln Gln Ala Ser Leu Ser
705 710 715

<210> 11

<211> 1920

<212> DNA

<213> Oryza sativa

<220>

<221> unsure

<222> (139)

<220>

<221> unsure

<222> (238)

<220>

<221> unsure

<222> (431)

<400> 11

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cgtcggccac ggaacactcc acgtcgccgg cgccgcacc ggcgacttca actaccttt 240
cgcgccgtcc aaggggggca agttcggtct cgcgcattcgag gacaccgact tcgagaggtc 300
caccaagaag tccgaggagg ccgtgctcag tgacctcgcc tggctcgcc ttgactggaa 360
cgaaggcccg gatgtcggtg gggatatgg gcccgcgc cagtccgagc gcaattcgat 420
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<210> 12
<211> 555
<212> PRT
<213> Oryza sativa

<220>
<221> UNSURE
<222> (130)

<400> 12
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20 25 30

His Arg Thr Ala Pro Ala Ala Arg Cys Gly Pro Val Arg Ala Val Ala
35 40 45

Asp Gly Asn Leu His Val Gly Gly Ala Arg Thr Ala His Phe Asn Tyr
50 55 60

Leu Phe Ala Arg Ser Lys Gly Gly Lys Phe Val Leu Arg Ile Glu Asp
65 70 75 80

Thr Asp Phe Glu Arg Ser Thr Lys Lys Ser Glu Glu Ala Val Leu Ser
85 90 95

Asp Leu Ala Trp Leu Gly Leu Asp Trp Asp Glu Gly Pro Asp Val Gly
100 105 110

Gly Glu Tyr Gly Pro Asp Arg Gln Ser Glu Arg Asn Ser Met Tyr Lys
115 120 125

Gln Xaa Ala Glu Lys Leu Met Glu Ser Gly Ala Val Tyr Gln Cys Phe
130 135 140

Tyr Ser Ser Glu Gly Leu Glu Gln Met Lys Glu Thr Ala Ser Arg Cys
145 150 155 160

Asn Leu Pro Pro Val Tyr Ile Gly Lys Trp Gly Thr Ala Ser Asp Ala
165 170 175

Glu Ile Gln Gln Glu Leu Glu Lys Gly Thr Pro Tyr Thr Tyr Arg Phe
180 185 190

Arg Val Pro Lys Glu Gly Ser Leu Lys Ile Asn Asp Leu Ile Arg Gly
195 200 205

Glu Val Ser Trp Asn Leu Asp Thr Leu Gly Asp Phe Val Ile Met Arg
210 215 220

Ser Asn Gly Gln Pro Val Tyr Asn Phe Cys Val Thr Val Asp Asp Ala
225 230 235 240

Thr Met Arg Ile Ser His Val Ile Arg Ala Glu Glu His Leu Pro Asn
245 250 255

Thr Leu Arg Gln Ala Leu Ile Tyr Lys Ala Leu Gly Phe Pro Met Pro
260 265 270

Ser Phe Ala His Val Ser Leu Ile Leu Ala Pro Asp Arg Ser Lys Leu
275 280 285

Ser Lys Arg His Gly Ala Thr Ser Val Gly Gln Tyr Lys Glu Met Gly
290 295 300

Tyr Leu Pro Gln Ala Met Val Asn Tyr Leu Ala Leu Leu Gly Trp Gly
305 310 315 320

Asp Gly Thr Glu Asn Glu Phe Phe Thr Ile Asp Asp Leu Val Glu Lys
325 330 335

Phe Thr Ile Asn Arg Val Asn Lys Ser Gly Ala Val Phe Asp Ala Val
340 345 350

Lys Leu Lys Trp Met Asn Gly Gln His Leu Arg Ser Phe Pro Pro Asp
355 360 365

Val Leu Ile Lys Ser Phe Glu Asp Arg Trp Lys Asp Thr Gly Ile Leu
370 375 380

Gln Glu Ser Glu Ser Gly Phe Ala Lys Glu Ala Ala Glu Leu Leu Lys
385 390 395 400

Asp Gly Ile Asp Leu Ile Thr Asp Ala Asp Ala Leu Ser Asn Leu
405 410 415

Leu Ser Tyr Pro Leu His Ala Thr Leu Ser Ser Asp Glu Ala Lys Ser
420 425 430

Val Val Gln Asp Lys Leu Ser Glu Val Ala Ser Gly Leu Ile Ser Ala
435 440 445

Tyr Asp Ser Gly Glu Leu Cys Gln Ala Leu Ala Glu Gly Arg Asp Gly
450 455 460

Trp Gln Lys Trp Val Lys Ile Phe Gly Lys Ser Leu Lys Arg Lys Gly
465 470 475 480

Lys Ser Leu Phe Met Pro Leu Arg Val Leu Leu Thr Gly Lys Leu His
485 490 495

Gly Pro Asp Met Gly Gly Thr Val Val Leu Ile His Lys Ala Gly Thr
500 505 510

Cys Gly Ala Val Thr Gln Gln Ser Gly Phe Val Asn Leu Asp Glu Arg
515 520 525

Phe Arg Ile Leu Lys Glu Val Glu Trp Glu Ser Leu Val Gln Glu Gln
530 535 540

Glu Ser Pro Ala Glu Thr Ala Val Pro Ala Ser
545 550 555

<210> 13

<211> 731

<212> DNA

<213> Glycine max

<400> 13

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tttctcaagt ctctgctctc tccgaacaac caccaccgt tcgcgttcgt ttgcgtccctt 180
ctccccaccgg aaacacctcac gtcggcggtg cccgaacggc cctcttcaac tacttggtcg 240
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aagggcctgg tggggaggg gattatggtc cttataggca gtctgatagg aattcttat 420
acaagcaatt tgcggataac ctacaccaat ccggcatgt ttatcgctgc ttctgttcta 480
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caggttaatg gcccagtgc acaaattgagg aagtagaaga agagctagca aaaggaactc 600
cttacactta ccgggttccga gtcctaaag gaagttaaa aattaatgat caaatacgag 660
gcgaagttag ttggaacttg gatacgcttg gagattttgt gataatgagg agtaatggtc 720
agcctgttta t 731

<210> 14

<211> 404

<212> PRT

<213> Glycine max

<400> 14

Val Arg Val Arg Phe Ala Pro Ser Pro Thr Gly Asn Leu His Val Gly
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Gly Ala Arg Thr Ala Leu Phe Asn Tyr Leu Phe Ala Arg Ser Lys Gly
20 25 30

Gly Lys Phe Val Leu Arg Ile Glu Asp Thr Asp Leu Glu Arg Ser Thr
35 40 45

Arg Glu Ser Glu Glu Ala Met Leu Lys Asp Leu Ser Trp Leu Gly Leu
50 55 60

Asp Trp Asp Glu Gly Pro Gly Val Gly Gly Asp Tyr Gly Pro Tyr Arg
65 70 75 80

Gln Ser Asp Arg Asn Ser Leu Tyr Lys Gln Phe Ala Asp Asn Leu His
85 90 95

Gln Ser Gly His Val Tyr Arg Cys Phe Cys Ser Asn Glu Glu Leu Glu
100 105 110

Lys Met Lys Glu Asp Ala Lys Leu Lys Gln Leu Pro Pro Val Tyr Thr
115 120 125

Gly Lys Trp Ala Ser Ala Thr Asn Glu Glu Val Glu Glu Glu Leu Ala
130 135 140

Lys Gly Thr Pro Tyr Tyr Arg Phe Arg Val Pro Lys Gly Ser Leu
145 150 155 160

Lys Ile Asn Asp Gln Ile Arg Gly Glu Val Ser Trp Asn Leu Asp Thr
165 170 175

Leu Gly Asp Phe Val Ile Met Arg Ser Asn Gly Gln Pro Val Tyr Asn
180 185 190

Phe Cys Val Thr Val Asp Asp Ala Thr Met Ala Ile Ser His Val Ile
195 200 205

Arg Ala Glu Glu His Leu Pro Asn Thr Leu Arg Gln Ala Leu Ile Tyr
210 215 220

Lys Ala Leu Gly Phe Pro Met Pro His Phe Ala His Val Ser Leu Ile
225 230 235 240

Leu Ala Pro Asp Arg Ser Lys Leu Ser Lys Arg His Gly Ala Thr Ser
245 250 255

Val Gly Gln Phe Arg Asp Met Gly Tyr Leu Pro Gln Ala Met Val Asn
260 265 270

Tyr Leu Ala Leu Leu Gly Trp Gly Asp Gly Thr Glu Asn Glu Phe Phe
275 280 285

Thr Leu Glu Gln Leu Val Glu Lys Phe Thr Ile Glu Arg Val Asn Lys
290 295 300

Ser Gly Ala Ile Phe Asp Ser Thr Lys Leu Arg Trp Met Asn Gly Gln
305 310 315 320

His Leu Arg Ser Leu Pro Ser Glu Glu Leu Asn Arg Ile Ile Gly Glu
325 330 335

Arg Trp Lys Asp Ala Gly Ile Ala Thr Glu Ser Gln Gly Ile Phe Ile
340 345 350

Gln Asp Ala Val Leu Leu Lys Asp Gly Ile Asp Leu Ile Thr Asp
355 360 365

Ser Glu Lys Ala Leu Ser Ser Leu Leu Ser Tyr Pro Leu Tyr Glu Thr
370 375 380

Leu Ala Ser Ala Glu Gly Lys Pro Ile Leu Glu Asp Gly Val Ser Glu
385 390 395 400

Val Ala Lys Ser

<210> 15
<211> 407

<212> DNA
<213> Triticum aestivum

<220>
<221> unsure
<222> (14)

<220>
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<400> 15

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gacacagatn agtcaaggac tgttccctggc gcgattgaaa aactctgcgc tgntttgaga 300
tgggggggtt taaaaaggga taaaaagggtt ggcccccaat ngaccgcaan ngggccttcc 360
aaaaatctca aaagactttt aangttataa aaaaaaacnc nccataa 407

<210> 16
<211> 79
<212> PRT
<213> Triticum aestivum

<220>
<221> UNSURE
<222> (55)

<220>
<221> UNSURE
<222> (69)

<400> 16

Lys Phe Gln Asn Ser Leu Ser Glu Arg Leu Pro Ala Arg Thr Arg Phe
1 5 10 15

Ala Pro Ser Pro Thr Gly Asn Leu His Leu Gly Ser Leu Arg Thr Ala
20 25 30

Leu Phe Asn Tyr Leu Ile Ala Lys Ala Thr Arg Gly Lys Phe Ile Leu
35 40 45

Arg Ile Glu Asp Thr Asp Xaa Ser Arg Thr Val Pro Gly Ala Ile Glu
50 55 60

Lys Leu Cys Ala Xaa Leu Arg Trp Gly Gly Leu Lys Arg Asp Lys
65 70 75

<210> 17

<211> 2387

<212> DNA

<213> Zea mays

<400> 17

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gcgggcgctg catgtcttaa tgcgcatcga gctcaacgca cccgtcaaat tggggaaagag 180
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gtacaaccac ttgctcaagt tcagggactt tcttcgttgg gaagcagctg tggccatggc 480
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cagtgttaact gagaagccac tggctggtgg ggacaaaagca aagggtgaca agaagagcaa 600
gaagaagaaaa actttgggtt aagggtacttc tgctgtgtc atgtgtctt gggaccatgt 660
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<210> 18
<211> 495
<212> PRT
<213> Zea mays

<400> 18

Met Leu Leu Arg Asp His Val Thr Asn Gly Ser Thr Val Ala Ala Met
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Asn Ser Ala Ser Val Ala Glu Trp Ala Thr Ser Leu Ser Leu Leu Phe
20 25 30

Asp Pro Lys Cys Pro Gly Leu Glu Ser Leu Val Glu Lys Val Lys Glu
35 40 45

Ile Val Glu Ser Asn Glu Val Arg Arg Leu Pro Lys Ile Pro Lys Gly
50 55 60

Thr Arg Asp Phe Gly Lys Glu Gln Met Ala Ile Arg Glu Arg Ala Phe
65 70 75 80

Ser Ile Ile Thr Ser Val Phe Lys Met His Gly Ala Thr Ala Leu Asp
85 90 95

Thr Pro Val Phe Glu Leu Arg Glu Thr Leu Met Gly Lys Tyr Gly Glu
100 105 110

Asp Ser Lys Leu Ile Tyr Asp Leu Ala Asp Gln Gly Glu Leu Cys
115 120 125

Ser Leu Arg Tyr Asp Leu Thr Val Pro Phe Ala Arg Tyr Val Ala Met
130 135 140

Asn Ser Ile Ser Ala Leu Lys Arg Tyr Gln Ile Ala Lys Val Tyr Arg
145 150 155 160

Arg Asp Asn Pro Ser Lys Gly Arg Tyr Arg Glu Phe Tyr Gln Cys Asp
165 170 175

Phe Asp Ile Ala Gly Val Tyr Glu Pro Met Glu Pro Asp Phe Glu Val
180 185 190

Ile Lys Val Leu Thr Glu Leu Leu Asn Gln Leu Asp Ile Gly Thr Tyr
195 200 205

Glu Ile Lys Leu Asn His Arg Lys Leu Leu Asp Gly Met Leu Glu Ile
210 215 220

Cys Gly Val Pro Pro Gln Lys Phe Arg Thr Val Cys Ser Ser Ile Asp
225 230 235 240

Lys Leu Asp Lys Gln Thr Phe Glu Gln Val Lys Lys Glu Leu Val Asp
245 250 255

Glu Lys Gly Ile Ser Asn Glu Thr Ala Asp Glu Ile Gly Asn Leu Val
260 265 270

Lys Thr Arg Gly Pro Pro Leu Glu Val Leu Met Glu Leu Arg Lys Glu
275 280 285

Gly Ser Lys Phe Met Asn Asn Val Gly Ser Val Ala Ala Leu Asn Glu
 290 295 300
 Leu Glu Ile Leu Phe Lys Ala Leu Asp Lys Ala Asn Ala Ile Ser Lys
 305 310 315 320
 Ile Thr Phe Asp Leu Ser Leu Ala Arg Gly Leu Asp Tyr Tyr Thr Gly
 325 330 335
 Val Ile Tyr Glu Ala Val Phe Lys Gly Ala Ala Gln Val Gly Ser Ile
 340 345 350
 Ala Ala Gly Gly Arg Tyr Asp Asn Leu Val Gly Met Phe Ser Gly Lys
 355 360 365
 Gln Ile Pro Ala Val Gly Val Ser Leu Gly Ile Glu Arg Val Phe Ala
 370 375 380
 Ile Met Glu Gln Gln Glu Lys Glu Arg Asn Glu Lys Ile Arg Pro Thr
 385 390 395 400
 Glu Thr Glu Val Leu Val Ser Ile Leu Gly Lys Asp Leu Thr Leu Ala
 405 410 415
 Ala Glu Leu Val Ser Glu Leu Trp Asn Ala Gly Ile Lys Ala Glu Phe
 420 425 430
 Lys Leu Thr Thr Arg Val Ala Asn His Ile Lys Tyr Ala Leu Gln Ser
 435 440 445
 Ser Ile Pro Trp Met Val Leu Val Gly Glu Ser Glu Leu Gln Lys Gly
 450 455 460
 Thr Val Lys Leu Lys Asp Val Glu Ala Asn Gln Glu Glu Glu Val Asp
 465 470 475 480
 Arg Lys Asp Phe Val Arg Glu Leu Lys Lys Arg Leu Ser Lys Ser
 485 490 495
 <210> 19
 <211> 754
 <212> DNA
 <213> Glycine max
 <220>
 <221> unsure
 <222> (18)
 <220>
 <221> unsure
 <222> (610)
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 <221> unsure
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 <221> unsure
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<220>
<221> unsure
<222> (740)

<400> 19
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GTCGAAAGGT TCTGCAAGAA GTTAAATT GTTATTCACT ACCAGAAAAT TTATTTGGCA 180
AGGTCTGCCT CATTATTGAT AAAATTGAGA AAATTCCAGC TGACGAGATA AAGAAAGAGT 240
TGAAAGCTGT TGGTCTATCT CAAGAGGCTG TCCAGGAGCT ATTGCAAGTC CTTCCTGTGA 300
AGTCATTGAC CGAGTTAGAA GAGAGACTG GGAGCAGTGG GGAAGCAGTT GCTGATCTGA 360
AACAGCTATT CTCCCTTGCT GAAAAAATTG GTTACTCTAA ATGGCTTCAA TTTGATGCT 420
CAGTTGTTGCG AGGTCTTGCT TACTACACTG GCATTGTATT TGAGGGTTT GACCAGAG 480
GAAAGCTGCG AGCTATCTGT GGTGGTGGTC GATATGATCA TTTGTTCTCA ACTTTGGTG 540
CTGATGACAT TGTGATGT GGTGGAT TTGGTGTGATGC AAGTCATAGT GGAATTGCTC 600
AAAAGAGAAAN GGTCTGTTAC CGGGAAAGCTT AACTTGCAAA TAGATGACAT TGTGTGTGCC 660
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GGCAAATTGT TGAAGTTGGN TTTGGGAAAAA CAAA 754

<210> 20
<211> 243
<212> PRT
<213> Glycine max

<220>
<221> UNSURE
<222> (6)

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<221> UNSURE
<222> (203)

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<222> (235)

<220>
<221> UNSURE
<222> (238)

<400> 20
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Ile Ala Ser Ile Val Thr Leu Phe Lys Arg Ile Gly Ile Thr Glu Ser
20 25 30

Asp Val Gly Phe Lys Val Ser Ser Arg Lys Val Leu Gln Glu Val Leu
35 40 45

Asn Cys Tyr Ser Val Pro Glu Asn Leu Phe Gly Lys Val Cys Val Ile
50 55 60

Ile Asp Lys Ile Glu Lys Ile Pro Ala Asp Glu Ile Lys Lys Glu Leu
65 70 75 80

Lys Ala Val Gly Leu Ser Gln Glu Ala Val Gln Glu Leu Leu Gln Val
85 90 95

Leu Ser Val Lys Ser Leu Thr Glu Leu Glu Glu Arg Leu Gly Ser Ser
100 105 110

Gly Glu Ala Val Ala Asp Leu Lys Gln Leu Phe Ser Leu Ala Glu Lys
115 120 125

Ile Gly Tyr Ser Lys Trp Leu Gln Phe Asp Ala Ser Val Val Arg Gly
130 135 140

Leu Ala Tyr Tyr Thr Gly Ile Val Phe Glu Gly Phe Asp Arg Glu Gly
145 150 155 160

Lys Leu Arg Ala Ile Cys Gly Gly Arg Tyr Asp His Leu Phe Ser
165 170 175

Thr Phe Gly Ala Asp Asp Ile Ala Ala Cys Gly Phe Gly Phe Gly Asp
180 185 190

Ala Ser His Ser Gly Ile Ala Gln Lys Arg Xaa Val Cys Tyr Arg Glu
195 200 205

Ala Leu Ala Asn Arg His Cys Val Cys Leu Gly Pro Lys Ile Phe Lys
210 215 220

Gly Cys Ala Ala Met Gly Pro Asn Asn Leu Xaa Glu Lys Xaa Gln Ile
225 230 235 240

Val Glu Val

<210> 21

<211> 1164

<212> DNA

<213> Triticum aestivum

<400> 21

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gtcatctgaa gcagtacagg gcatcattga agtgtctctt ctcaagtcac tgtccaaact 240
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aaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa 1140
aaaaaaaaaaa aaaaaaaaaaaa aaaa 1164

<210> 22

<211> 271

<212> PRT

<213> Triticum aestivum

<400> 22

Lys Leu Gly Ile Thr Ser Ser Asp Val Gly Ile Arg Leu Ser Ser Arg
1 5 10 15

Lys Val Leu Gln Ala Val Leu Asp Met Tyr Ser Val Pro Gln His Leu
20 25 30

Phe Thr Gln Val Cys Val Ile Val Asp Lys Leu Gly Lys Leu Ser Arg
35 40 45

Glu Glu Ile Glu Lys Glu Leu Ile Ser Thr Gly Leu Ser Ser Glu Ala
50 55 60

Val Gln Gly Ile Ile Glu Val Leu Ser Leu Lys Ser Leu Ser Lys Leu
65 70 75 80

Glu Glu Val Leu Gly Ser Gly Val Glu Ala Val Ala Asp Leu Lys Lys
85 90 95

Leu Phe Ser Leu Ala Glu Gln Tyr Gly Tyr Ser Asp Trp Ile Cys Phe
100 105 110

Asp Ala Ser Val Val Arg Gly Leu Ala Tyr Tyr Thr Gly Ile Val Phe
115 120 125

Glu Ala Phe Asp Arg Glu Gly Glu Leu Arg Ala Ile Cys Gly Gly
130 135 140

Arg Tyr Asp Arg Leu Leu Ser Thr Phe Gly Thr Glu Asp Val Pro Ala
145 150 155 160

Cys Gly Phe Gly Phe Gly Asp Ala Val Ile Val Glu Leu Leu Lys Glu
165 170 175

Lys Gly Leu Leu Pro Asp Leu Pro Arg Gln Ile Asp Asp Ile Val Phe
180 185 190

Pro Leu Asp Glu Glu Leu Glu Gly Pro Ala Ser Ser Val Ala Ser Cys
195 200 205

Leu Arg Lys Lys Gly Arg Ser Val Asp Leu Val Glu Asp Lys Arg Leu
210 215 220

Lys Trp Val Phe Lys His Ala Glu Arg Ile Asn Ala Ser Arg Leu Ile
225 230 235 240

Leu Val Gly Lys Ser Glu Trp Glu Arg Gly Met Val Arg Val Lys Ile
245 250 255

Leu Ser Thr Arg Glu Glu Phe Glu Val Lys Ala Gly Glu Leu Gln
260 265 270

<210> 23

<211> 913

<212> DNA

<213> Zea mays

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tcaatgttga gcaggcagag tggatcatat atgttacaga tggttgtcag cagcagcact 240
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ttccgaaccc gcagttactga ggttgcgtca ttggtagagc tacttgcata ggctaaatct 420
cgtagccaaat cagaactact acaacggctc actggaaaatg gcaaaattgt tgactggacg 480
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ctaaaaaaata acaggctcac taattacaca ttttagtttg aacaaatgct gagcgataag 600
ggaaatactg ctgtgtaccc tcagttatgc catgctcgta tttgttccat tattcgaaaa 660
tccaacaaga acgtggnaga ctgaagagat ggagccatct ctctcgacca tccggattag 720
cgctgttgg gctgttatctt anccgatttg cagagttttt gaagaggatc acgaactact 780
ccaaattttgt gtgtgaatac tgtcaatcan ctgaaagtca caanatcata caactgcaag 840
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ctcgatcna cat 913

<210> 24
<211> 221
<212> PRT
<213> Zea mays

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<220>
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<222> (96)

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<222> (156)

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<400> 24
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Gly Leu Ile Lys Glu Ser Glu Gly Ala Arg Val Ile Phe Ile Gln Gly
20 25 30

His Gln Ile Pro Leu Ile Val Val Lys Ser Asp Gly Gly Phe Asn Tyr
35 40 45

Ala Ser Thr Asp Leu Thr Ala Leu Trp Tyr Arg Leu Asn Val Glu Gln
50 55 60

Ala Glu Trp Ile Ile Tyr Val Thr Asp Val Gly Gln Gln His Phe
65 70 75 80

Asp Met Val Phe Ser Ala Ala Lys Met Ala Gly Trp Leu Pro Asp Xaa
85 90 95

Glu Lys Lys Phe Pro Lys Thr Ser His Val Gly Phe Gly Leu Phe Leu
100 105 110

Val Gln Asp Gly Lys Arg Phe Arg Thr Arg Ser Thr Glu Val Val Arg
115 120 125

Leu Val Glu Leu Leu Asp Glu Ala Lys Ser Arg Ser Lys Ser Glu Leu
130 135 140

Thr Glu Asn Gly Lys Ile Val Asp Trp Thr Asp Xaa Glu Leu Glu Gln
145 150 155 160

Thr Ser Glu Ala Val Gly Tyr Gly Ala Val Lys Tyr Ala Asp Leu Lys
165 170 175

Asn Asn Arg Leu Thr Asn Tyr Thr Phe Ser Phe Glu Gln Met Leu Ser
180 185 190

Asp Lys Gly Asn Thr Ala Val Tyr Leu Gln Tyr Ala His Ala Arg Ile
195 200 205

Cys Ser Ile Ile Arg Lys Ser Asn Lys Asn Val Xaa Asp
210 215 220

<210> 25
<211> 551
<212> DNA
<213> Oryza sp.

<220>
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<400> 25
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gcaacaaact tccgttaaccc catggcagtt gggcaggcaa ttgcaaataa cctccccca 240
tcaaatatta tccaatccat ctctgttgcc gganctgggt acattaacat aacgttatcc 300
agcaatttggaa ttgcacagag gataaaaaa catgcttgggt tttgggaatc aaaacatggg 360
gaacaatcct taacctgttt aagaaggcaa ntgctggntt tttcaanccc caataattgc 420
aaaaagaana tcaagttgg gcaataatna aggncaacaa taaatngggg natanccaa 480
ctcaaaaangg ttngggntca caaaanggtt aanttcntn acgtaaaacan gttgggaaac 540
nggggnacac a 551

<210> 26
<211> 68
<212> PRT
<213> Oryza sp.

<220>
<221> UNSURE
<222> (51)

<400> 26
Phe Gly Asp Tyr Gln Cys Asn Asn Ala Met Ser Val Phe Ser Arg Ile
1 5 10 15

Arg Gly Ser Ala Thr Asn Phe Arg Asn Pro Met Ala Val Gly Gln Ala
20 25 30

Ile Ala Asn Asn Leu Pro Gln Ser Asn Ile Ile Glu Ser Ile Ser Val
35 40 45

Ala Gly Xaa Gly Tyr Ile Asn Ile Thr Leu Ser Ser Asn Trp Ile Ala
50 55 60

Gln Arg Ile Gln
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<210> 27
<211> 411

<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (18)

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<222> (35)

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<400> 27
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tatgttacag atattggca gcaacagcac tttgatatnc tattnaaggc ctataggcgt 180
gcaggttggt taccaaagga tgagaatgcg tatccaaat gtactcatat aggtttggt 240
cttgttcgtt gggaaatgg aaaacgattt cggactcgca ncagtnangt tgttcgatta 300
gttgattact ttagtgcgct aaaangcgct gtaaaattgc cttttgaaa cgtgatacaa 360
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<210> 28
<211> 115
<212> PRT
<213> Glycine max

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<222> (6)

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<221> UNSURE
<222> (109)

<400> 28

Val Glu Gly Val Asp Xaa Pro Leu Ile Ala Val Xaa Arg Asp Gly Gly
1 5 10 15

Xaa Asn Tyr Phe Thr Asp Leu Ala Ser Leu Trp Tyr Arg Leu Asn
20 25 30

Glu Glu Lys Leu Glu Trp Ile Val Tyr Val Thr Asp Ile Gly Gln Gln
35 40 45

Gln His Phe Asp Xaa Leu Xaa Lys Ala Tyr Arg Arg Ala Gly Trp Leu
50 55 60

Pro Lys Asp Glu Asn Ala Tyr Pro Lys Cys Thr His Ile Gly Phe Gly
65 70 75 80

Leu Val Leu Gly Glu Asp Gly Lys Arg Phe Arg Thr Arg Xaa Ser Xaa
85 90 95

Val Val Arg Leu Val Asp Tyr Leu Met Lys Leu Lys Xaa Ala Val Lys
100 105 110

Leu Pro Ser
115

<210> 29
<211> 565

<212> DNA
<213> Triticum sp.

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<400> 29
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ctcgtagtac tgaggttgtt cgggtggaa gacctacttg atgaggctaa atctcgaagt 180
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gaaggaacta agagcaaact tcaaaaggca gtaagatatg gcgcgtgtcaa agtatgcggg 300
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caacatggtg tnnaaaaacta aaangatggg anattccncc tgccanccaa atagctgcct 480
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aaactatnac taccnaagta aaagt 565

<210> 30
<211> 33
<212> PRT
<213> Triticum sp.

<400> 30
Glu Lys Lys Phe Pro Lys Thr Ser His Val Gly Phe Gly Leu Val Leu
1 5 10 15

Gly Ala Asp Gly Lys Arg Phe Arg Thr Arg Ser Thr Glu Val Val Arg
20 25 30

Leu

<210> 31
<211> 546
<212> DNA
<213> Oryza sp.

<220>
<221> unsure
<222> (448)

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<400> 31
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catcgatttg atcaactgatg ctgacgcagc cctttcaaac ctgttgcgt atcccctcca 180

tgctacatta agcagtatg aagctaaatc tgggtgcaa gacaagctt ctgagggtgc 240
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tgatgggtgg cagaagtggg tgaaaatttt tggcaaatca cttaaaagaa agggaaagtc 360
actctttatg ccgctccgtg tactgctgac tggcaagctt catgggcctg acatgggcgg 420
caccgtatgc ctcatacaca aagccgnac tggagcgg tcactcaaca atccggttc 480
gtaaatctcg acgagaggc agaattctga angagtggag tggagtcaact ggtacaggac 540
aagatc 546

<210> 32
<211> 147
<212> PRT
<213> Oryza sp.

<400> 32

Pro Pro Asp Val Leu Ile Lys Ser Phe Glu Asp Arg Trp Lys Asp Thr
1 5 10 15

Gly Ile Leu Gln Glu Ser Glu Ser Gly Phe Ala Lys Glu Ala Ala Glu
20 25 30

Leu Leu Lys Asp Gly Ile Asp Leu Ile Thr Asp Ala Asp Ala Ala Leu
35 40 45

Ser Asn Leu Leu Ser Tyr Pro Leu His Ala Thr Leu Ser Ser Asp Glu
50 55 60

Ala Lys Ser Val Val Gln Asp Lys Leu Ser Glu Val Ala Ser Gly Leu
65 70 75 80

Ile Ser Ala Tyr Asp Ser Gly Glu Leu Cys Gln Ala Leu Ala Glu Gly
85 90 95

Arg Asp Gly Trp Gln Lys Trp Val Lys Ile Phe Gly Lys Ser Leu Lys
100 105 110

Arg Lys Gly Lys Ser Leu Phe Met Pro Leu Arg Val Leu Leu Thr Gly
115 120 125

Lys Leu His Gly Pro Asp Met. Gly Gly Thr Val Val Leu Ile His Lys
130 135 140

Ala Gly Thr
145

<210> 33
<211> 524
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (386)

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<222> (459)

<220>
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<222> (481)

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<222> (483)

<220>
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<222> (486)

<400> 33
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tctccgaaca accaccaccc gttcgcgttc gtttcgctcc ttctcccacc ggaaacctcc 180
acgtcggcgg tgccccaaacg gccccttca actacttgtt cgcaagggtcc aaaggtggga 240
aatttgtgct gagaatttag gacactgact tggagaggtc caagtaggga gtctgaggag 300
gccatgctca aagatcttc ttggcttggg cttgattggg atgaagggcc tgggtgttgg 360
aggggattat ggtccttaaa aggcantctg agaaggaatt ccttatacaa acaatatgcc 420
ggngaaacta cacaatccg ggcaagtta accgctgcnt tctggtccaa agagggact 480
nanagnaaat gaaaggaggt tgctaaacta aagcaactgg cccc 524

<210> 34
<211> 94
<212> PRT
<213> Glycine max

<220>
<221> UNSURE
<222> (63)

<400> 34
Gln Arg Arg Arg Phe Ser Val Ser Ala Leu Ser Glu Gln Pro Pro Pro
1 5 10 15

Val Arg Val Arg Phe Ala Pro Ser Pro Thr Gly Asn Leu His Val Gly
20 25 30

Gly Ala Arg Thr Ala Leu Phe Asn Tyr Leu Phe Ala Arg Ser Lys Gly
35 40 45

Gly Lys Phe Val Leu Arg Ile Glu Asp Thr Asp Leu Glu Arg Xaa Ser
50 55 60

Arg Glu Ser Glu Glu Ala Met Leu Lys Asp Leu Ser Trp Leu Gly Leu
65 70 75 80

Asp Trp Asp Lys Gly Leu Gly Val Gly Gly Asp Tyr Gly Pro
85 90

<210> 35
<211> 506
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (18)

<220>
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 <222> (483)

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 <222> (505)

<220>
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 <222> (506)

<400> 35
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 gtcgaaaagggt tctgcaagaa gtattaaatt gttattcagt accagaaaat ttatttggca 180
 aggtctgcgt cattattgat aaaattgaga aaattccagc tgacgagata aagaaagagt 240
 tgaaaagctgt tggcttatct caagaggctg tccaggagct attgcaagtc ctttctgtga 300
 agtcattgac cgagtttagaa gagagacttg ggagagtggg gaagcagttg ctgatctgaa 360
 acagtattct cccttgctga aaaaattgggt tactctaaat ggttcaattt gatgatagtt 420
 gttcgaggtc ttgcttacta cactggcatt gatttgaggg tttgacgaga ggaagctgca 480
 gcntctgtgt gtgtcaatac attgnn 506

<210> 36
 <211> 48
 <212> PRT
 <213> Glycine max

<400> 36
 Asp Val Gly Phe Lys Val Ser Ser Arg Lys Val Leu Gln Glu Val Leu
 1 5 10 15

Asn	Cys	Tyr	Ser	Val	Pro	Glu	Asn	Leu	Phe	Gly	Lys	Val	Cys	Val	Ile
							20		25				30		

Ile	Asp	Lys	Ile	Glu	Lys	Ile	Pro	Ala	Asp	Glu	Ile	Lys	Lys	Glu	Leu
							35		40			45			

<210> 37
 <211> 577
 <212> DNA
 <213> Triticum sp.

<220>
 <221> unsure
 <222> (140)

<220>
 <221> unsure
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<220>
 <221> unsure
 <222> (411)

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<221> unsure
<222> (564)

<400> 37.
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aagctggga aactgagtag ggaagaaatt gagaaggaat tgatttcaac tgggctgtca 180
tctgaagcag tacagggcat cattgaagtg ctctctctca agtcactgtc caaacttcaa 240
gaggtgctag gctcaggtgt tgaagccgtt gctgacttga agaaccttctt ctcgcttgct 300
gagcaatatg gttattctga ttggatctgt ttcatgtcat ctgttggatcg tggccttgca 360
tactacacan ggattgttt ttgaggctt tgataggaa gggaaacttga nancatttgt 420
ggtggggggg agtatgaca ggctacgtca acatttgaa ctgaagatnt ccaccctgtg 480
nctttggatt tgaatcctg tcanagtggc ctccnaaaga aaggctttt ctacctgcac 540
tcaaataata nattgtcca ttgncaagac ttgggggg 577

<210> 38
<211> 46
<212> PRT
<213> Triticum sp.

<220>
<221> UNSURE
<222> (38)

<400> 38
Ile Arg Leu Ser Ser Arg Lys Val Leu Gln Ala Val Leu Asp Met Tyr
1 5 10 15

Ser Val Pro Gln His Leu Phe Thr Gln Val Cys Val Ile Val Asp Lys
20 25 30

Leu Gly Lys Leu Ser Xaa Glu Glu Ile Glu Lys Glu Leu Ile
35 40 45